



- 1 -

SEQUENCE LISTING

<110> Lipton, Stuart A.  
Okamoto, Shu-ichi

<120> Methods of Differentiating and  
Protecting Cells By Modulating the P38/MEF2 Pathway

<130> P-LJ 4714

<140> US 09/876,187

<141> 2001-06-05

<150> US 60/209,539

<151> 2000-06-05

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (415)...(1935)

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Met

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Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr  
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Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn  
35 40 45

RECEIVED  
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Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn	
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Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys Asp	
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Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu	
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aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat cat	801
Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn His	
115 120 125	
aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc aca	849
Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr	
130 135 140 145	
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Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly Ser	
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Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp Ser	
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Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser Pro	
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Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met Leu	
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Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro Val	
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Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly Ala	
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Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu Ser	
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His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly Gln	
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tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc agc	1617
Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile Ser	
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Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro Ser	
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<213> Homo sapiens

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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe  
35 40 45  
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys  
50 55 60  
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr  
65 70 75 80  
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys  
85 90 95  
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu  
100 105 110  
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn  
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His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val

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Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp					
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Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser					
	180		185		190
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met					
	195	200		205	
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro					
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Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly					
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Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro					
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Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp					
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Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu					
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Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro					
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Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr					
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Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly					
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Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln					
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Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly					
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Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile					
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Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro					
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Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro					
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Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln					
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Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser					
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Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro					
465		470		475	480
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cctcagcctg atcctggaag agactcgggg cccccagccc tccgccaacc cagacaaaga 420  
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Met Gly Arg Lys Lys Ile Gln Ile Ser Arg

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5

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Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys Arg Lys Phe  
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ggg ctg atg aag aag gcc tat gag ctg agc gtg ctc tgt gac tgt gag 568  
Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu  
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ata gcc ctc atc atc ttc aac agc gcc aac cgc ctc ttc cag tat gcc 616  
Ile Ala Leu Ile Ile Phe Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala  
45 50 55

agc acg gac atg gac cgt gtg ctg ctg aag tac aca gag tac agc gag 664  
Ser Thr Asp Met Asp Arg Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu  
60 65 70

ccc cac gag agc cgc acc aac act gac atc ctc gag acg ctg aag cgg 712  
Pro His Glu Ser Arg Thr Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg  
75 80 85 90

agg ggc att ggc ctc gat ggg cca gag ctg gag ccg gat gaa ggg cct 760  
Arg Gly Ile Gly Leu Asp Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro  
95 100 105

gag gag cca gga gag aag ttt cgg agg ctg gca ggc gaa ggg ggt gat 808  
Glu Glu Pro Gly Glu Lys Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp  
110 115 120

ccg gcc ttg ccc cga ccc cgg ctg tat cct gca gct cct gct atg ccc 856  
Pro Ala Leu Pro Arg Pro Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro  
125 130 135

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Ser Pro Asp Val Val Tyr Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro  
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Ser Gly Leu Gly Glu Ala Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe	
155 160 165 170	
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Arg Pro Ala Ala Pro Lys Ala Gly Pro Pro Gly Leu Val His Pro Leu	
175 180 185	
ttc tca cca agc cac ctc acc agc aag aca cca ccc cca ctg tac ctg	1048
Phe Ser Pro Ser His Leu Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu	
190 195 200	
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Pro Thr Glu Gly Arg Arg Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro	
205 210 215	
cga ggg gga cta aac acc tcc aga agc ctc tac agt ggc ctg cag aac	1144
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Pro Cys Ser Thr Ala Thr Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe	
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Leu Pro Gly Gly Pro Pro Val Gly Ala Glu Ala Trp Ala Arg Arg Val	
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Pro Gln Pro Ala Ala Pro Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser	
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Leu Ser Ala Ser Leu Arg Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg	
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Pro Ser Pro Ile Pro Cys Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys	
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Gly Leu Gly Pro Pro Cys Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro	
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gcg agg gca cgt ggg gac ccc acc tcc ctc cag gcc tct tca gag aag	1528
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Thr Gln Gln  
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Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr  
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Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys  
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Phe Arg Arg Leu Ala Gly Glu Gly Asp Pro Ala Leu Pro Arg Pro  
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Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr  
130 135 140  
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala  
145 150 155 160  
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys  
165 170 175  
Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu  
180 185 190  
Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg  
195 200 205  
Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr  
210 215 220  
Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr  
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Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro  
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275 280 285  
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<212> DNA

<213> Homo sapiens

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<222> (402)...(1820)

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gctgaagaag gagatttggt tggaggaaac aggaaagaga aagaaaagga aggaaaaaat 360
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                                         Met Gly Arg Lys Lys
                                         1             5

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Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn Arg Gln Val Thr Phe
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Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala Tyr Glu Leu Ser Val
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ctg tgt gac tgt gag att gcg ctg atc atc ttc aac agc acc aac aag 560
Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe Asn Ser Thr Asn Lys
                        40                45                50

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Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys Val Leu Leu Lys Tyr
                        55                60                65

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acg gag tac aac gag ccg cat gag agc cgg aca aac tca gac atc gtg 656
Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val
                        70                75                80                85

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gag acg ttg aga aag aag ggc ctt aat ggc tgt gac agc cca gac ccc 704
Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys Asp Ser Pro Asp Pro
                        90                95                100

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Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu Ser Glu Asp Lys Tyr

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120	125	130	
tgt gct gtt cca cct ccc aac ttc gag atg cca gtc tcc atc cca gtg			848
Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro Val Ser Ile Pro Val			
135	140	145	
tcc agc cac aac agt ttg gtg tac agc aac cct gtc agc tca ctg gga			896
Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro Val Ser Ser Leu Gly			
150	155	160	165
aac ccc aac cta ttg cca ctg gct cac cct tct ctg cag agg aat agt			944
Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser Leu Gln Arg Asn Ser			
170	175	180	
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Met Ser Pro Gly Val Thr His Arg Pro Pro Ser Ala Gly Asn Thr Gly			
185	190	195	
ggt ctg atg ggt gga gac ctc acg tct ggt gca ggc acc agt gca ggg			1040
Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala Gly Thr Ser Ala Gly			
200	205	210	
aac ggg tat ggc aat ccc cga aac tca cca ggt ctg ctg gtc tca cct			1088
Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly Leu Leu Val Ser Pro			
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ggt aac ttg aac aag aat atg caa gca aaa tct cct ccc cca atg aat			1136
Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser Pro Pro Pro Met Asn			
230	235	240	245
tta gga atg aat aac cgt aaa cca gat ctc cga gtt ctt att cca cca			1184
Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu Ile Pro Pro			
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Leu Asn Gln Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr			
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Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly			
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Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu			
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Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala  
330 335 340

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Ser Arg Tyr Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val  
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Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
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Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
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Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
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Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
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Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
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Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser

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Asp	Val	Asp	Leu	Leu	Leu	Asn	Gln	Arg	Ile	Asn	Asn	Ser	Gln	Ser	Ala				
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Leu Ile Ile Phe Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr	
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Glu Ser Arg Thr Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly	
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Phe Asn Gly Cys Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu	
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Gln Ser Pro Leu Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu	
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Val Ala Asn Gly Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro	
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ccc cca cct acc cac agc acc cag ctt gga gcc ccc agc cgc aag ccc	999
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Asp Leu Arg Val Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His	
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Pro Ser Leu Leu Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala	
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Tyr Asn Thr Asp Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro	
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Gln Gln Pro Pro Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln	
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Ser Tyr Glu Thr Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro  
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Tyr	Val	Ser	Ala	Arg	Ala	Ser	Pro	Gly	Leu	Leu	Pro	Val	Ala	Asn	Gly	225	230	235
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<213> Homo sapiens

<400> 19  
Leu Ser Ile Lys Ser Glu Pro Val Ser Pro Pro Arg Asp Arg  
1 5 10

<210> 20  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 20  
Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Cys Ser Ser Ser Tyr Gly  
1 5 10 15  
Asp Ser Asp Arg Glu Asp  
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<210> 21  
<211> 26  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> 9, 10, 11, 12, 13, 14, 15, 16, 17, 18  
<223> Xaa = Any Amino Acid

<400> 21  
Pro Ala Lys Ser Pro Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Arg Lys Pro Asp Leu Arg Val Ile  
20 25

<210> 22  
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<213> Homo sapiens

<400> 22  
Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu Ser Gln Gly Leu  
1 5 10 15  
Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp Tyr Gln Leu Pro  
20 25 30  
Ser Ala Glu Leu Ser Ser Leu  
35

<210> 23  
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<212> PRT  
<213> Homo sapiens

<400> 23  
Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu Arg  
1 5 10

<210> 24  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 24  
Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val Glu  
1 5 10